

### **REMARKS/ARGUMENTS**

With this amendment, claims 2, 3, and 16-26 are pending. New claim 27 is added. For convenience, the Examiner's rejections are addressed in the order presented in a September 2, 2004, Office Action.

#### **I. Status of the claims**

Claim 2 is amended to recite a recombinant nucleic acid that comprises a nucleic acid sequence having at least 98% identity to a reference sequence, *e.g.*, SEQ ID NO:1, 3, or 5. Claim 21 is amended to recite a recombinant nucleic acid that comprises a nucleic acid sequence having at least 99% identity to a reference sequence, *e.g.*, SEQ ID NO:1, 3, or 5. Support for these amendments is found throughout the specification, for example at page 18, lines 30-35. These amendments add no new matter.

Claim 16 is amended to recite a nucleic acid sequence that encodes a MINK3 protein having at least 98% identity to a reference sequence, *e.g.*, SEQ ID NO:2, 4, or 6. Claim 22 is amended to recite a nucleic acid sequence that encodes a MINK3 protein having at least 99% identity to a reference sequence, *e.g.*, SEQ ID NO:2, 4, or 6. Support for these amendments is found throughout the specification, for example at page 15, lines 1-7. These amendments add no new matter.

New claim 27 is added and is directed to a recombinant nucleic acid that comprises a nucleotide sequence complementary to the nucleic acid sequences of claims 2 or 16. Support for this amendment is found throughout the specification, for example at page 4, lines 29-32. This amendment adds no new matter.

#### **II. Rejections under 35 U.S.C. §112, first paragraph, written description**

Claims 2, 3, and 21 are rejected under 35 U.S.C. §112, first paragraph as allegedly containing subject matter that was not described in specification. The Office Action points out that the purpose of the written description requirement is to demonstrate that the inventors had possession of the claimed invention at the time of filing. The Office Action first objects to the

term "complement" in claims 2, 3 and 21, alleging, for example, that the Applicants are not in possession of a complementary strand of SEQ ID NO:1 that encodes a MINK3 protein. In order to expedite prosecution, claims 2, 3 and 21 are amended and no longer recite "complement" or similar terms. In view of these amendments, Applicants respectfully request withdrawal of the rejection under 35 U.S.C. §112, first paragraph.

### **III. Rejections under 35 U.S.C. §102(b)**

Claims 2, 3, 16-18, 19, 20, and 22-26 are rejected as allegedly anticipated by various references under 35 U.S.C. §102(b). To the extent the rejection applies to the amended claims, Applicants respectfully traverse the rejection.

To anticipate a claim, the reference must teach every element of the claim. "A claim is anticipated only if each and every element as set forth in the claim is found...in a single prior art reference." *Verdegaal Bros. v. Union Oil of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987). Thus, in order to anticipate, the cited references must contain every element of the claims at issue. The cited references do not.

The amended claims now recite 98% or 99% identity to a reference sequence. Applicants assert again the cited references fail to disclose all the elements of the amended claims. Moreover, at a minimum, claims directed to the exact reference sequences, *i.e.*, claims 3, and 23, are allowable. In addition, Applicants object to sequence alignments apparently used by the Office Action to find anticipation of the claims. As discussed below for each cited sequence, the sequence alignments were used incorrectly and some sequences were improperly cited as prior art.

#### **A. Rejection of claims 2, 3, and 16-18 in view of *Ippeita et al.***

Claims 2, 3, and 16-18 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by *Ippeita et al.*, *FEBS Letters* 469:19023 (2000). Applicants respectfully remind the Examiner that analysis of a claimed sequence must be performed on the entire sequence; using portions of a claimed sequence to obtain a finding of anticipation is improper. In addition,

references cannot be cited as prior art unless they were publicly available before the filing date of the present application.

For nucleic acid analysis, the Office Action compares a nucleic acid from Accession number AB03598 to SEQ ID NO:1 and alleges that over 96% identity is shared by the two sequences. This analysis is incorrect. The alignment sent with the Office Action improperly uses only a portion of the full length SEQ ID NO:1. Applicants submit as Exhibit A, an alignment between SEQ ID NO:1 and the nucleic acid sequence of Accession Number AB03598 demonstrating that the sequences share only 95.4% identity. Applicants submit that, using similar analysis, SEQ ID NO: 3 and 5 share less than 96% identity with the cited nucleic acid sequence. Thus, the % identity value cited by the Office Action is incorrect and the amended claims are not anticipated by the nucleotide sequence of Accession Number AB03598.

For amino acid sequence analysis, the Office Action improperly cites a sequence that was not publicly available until well after the filing date of the present application. The Office Action asserts that the MINK1 disclosure of Ippeita *et al.* is more than 99% identical to the claimed reference amino acid sequence. Unfortunately, the Office Action did not use the amino acid sequence discussed by Ippeita *et al.* to perform alignment analysis. The MINK1 amino acid sequence referred to in Ippeita *et al.* is found at Accession Number AB03598. *See, Ippeita et al.* at page 20, paragraph 2.10. Instead, the Office Action used an amino acid from Accession Number Q8N4C8. Applicants submit as Exhibit B an NCBI Sequence Revision History from the Entrez website, indicating that Accession Number Q8N4C8 was first seen at NCBI on April 1, 2003, well after the October 19, 2001 filing date of the present invention. Applicants submit as Exhibit C an alignment between the amino acid sequence of Accession Number AB03598 (*i.e.*, the sequence of Ippeita *et al.*) and SEQ ID NO:2 of the present invention. SEQ ID NO:2 and the amino acid sequence of Accession Number AB03598 share only 95.6% identity, and Applicants submit that, using similar analysis, SEQ ID NO: 4 and 6 also share less than 96% identity with the cited amino acid sequence. Thus, the claimed subject matter was not taught by a prior disclosure of properly cited MINK1 sequences.

*B. Rejection of claims 2, 3, and 16-18 in view of Plowman et al.*

Claims 2, 3, and 16-18 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by Plowman *et al.*, US Patent No. 6,656,716 ('716 patent). Again, Applicants respectfully remind the Examiner that analysis of a claimed sequence must be performed on the entire sequence; using portions of a claimed sequence to obtain a finding of anticipation is improper.

For nucleic acid analysis, Office Action compares SEQ ID NO:11 from the '716 patent to SEQ ID NO:1 of the present application and alleges that over 95% identity is shared by the two sequences. This analysis is incorrect. The alignment sent with the Office Action improperly uses only a portion of the full length SEQ ID NO:1 (*i.e.*, begins at nucleotide 110) and also truncates cited SEQ ID NO:11 (ending with nucleotide 3987 of 4133). Applicants submit as Exhibit D, an alignment between full length SEQ ID NO:1 and full length SEQ ID NO:11 from the '716 patent demonstrating that the sequences have only 90.2% identity. Applicants submit that, using similar analysis, SEQ ID NO: 3 and 5 also have identities of less than 95% to the cited nucleic acid reference sequence. Thus, the % identity value cited by the Office Action is incorrect and the amended claims are not anticipated by the nucleotide sequence of SEQ ID NO:11 from the '716 patent.

For amino acid analysis, Office Action compares SEQ ID NO:15 from the '716 patent to SEQ ID NO:2 of the present application and reports that over 95% identity is shared between the two sequences. This analysis is incorrect. The alignment sent with the Office Action improperly uses only a portion of the full length SEQ ID NO:2 (*i.e.*, begins at amino acid 36). Applicants submit as Exhibit E, an alignment between full length SEQ ID NO:2 and full length SEQ ID NO:15 from the '716 patent demonstrating that the sequences share only 93.3% identity. Applicants submit that, using similar analysis, SEQ ID NO: 3 and 5 also have identities of less than 95% to the cited nucleic acid reference sequence. Thus, the % identity value cited by the Office Action is incorrect and the amended claims are not anticipated by the nucleotide sequence of SEQ ID NO:15 from the '716 patent.

C. *Rejection of claims 19, 20, and 22-26 in view of Ippeita et al.*

Claims 19, 20, and 22-26 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by Ippeita *et al.* because, according to the Office Action, the reference discloses sequences with at least 96% identity to the claimed nucleic acid sequences and with at least 99% identity to the claimed amino acid sequences.

Applicants respectfully remind the Examiner that, in order to anticipate a claim, a reference must teach each and every element of the claim. Claims 19, 20, and 22-26 each directly or indirectly depend from claim 2. Thus, each claim recites an amino acid or a nucleic acid with at least 98% identity to a reference sequence. The deficiencies of Ippeita *et al.* are described in detail above, in particular, the failure of Ippeita *et al.* to teach nucleic acids with at least 98% identity to SEQ ID NO:1, 3, or 5 or amino acids with at least 98% identity to SEQ ID NO:2, 4, or 6. As Ippeiata *et al.* fail to teach the nucleic acid or amino acid sequences required by claims 19, 20, and 22-26, the reference cannot anticipate those claims.

In view of the above amendments and arguments, Applicants respectfully request withdrawal of the rejections under 35 U.S.C. §102(b).

**CONCLUSION**

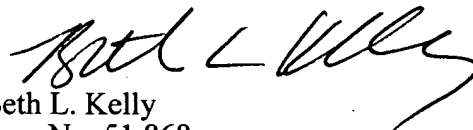
In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

Appl. No. 10/029,115  
Amdt. dated December 2, 2004  
Reply to *Final* Office Action of Sept. 2, 2004

PATENT

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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Attachments: Notice of Appeal  
Exhibits A-E

BLK:blk/jhd  
60366467 v1



# Align two sequences

Mon Nov 29 23:17:11 "GMT 2004"

```
/usr/tmp/seq1.292684.sca : 3951 nt
>SEQ ID NO:1, 3951 bases, A90814F5 checksum.      3951 nt vs.
>AB035698, 3888 bases, DC6FFDFE checksum.        3888 nt
scoring matrix: , gap penalties: -12/-2
95.4% identity;      Global alignment score: 14885
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```
      10      20      30      40      50      60
/usr/t GCCCTTATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG
      :
AB0356 -----ATGGGCGACCCAGCCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG
      10      20      30      40      50

      70      80      90     100     110     120
/usr/t CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG
      :
AB0356 CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG
      60      70      80      90     100     110

      130     140     150     160     170     180
/usr/t GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC
      :
AB0356 GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC
      120     130     140     150     160     170

      190     200     210     220     230     240
/usr/t ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC
      :
AB0356 ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC
      180     190     200     210     220     230

      250     260     270     280     290     300
/usr/t CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGAAACGAT
      :
AB0356 CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGAAACGAT
      240     250     260     270     280     290

      310     320     330     340     350     360
/usr/t GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG
      :
AB0356 GACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG
      300     310     320     330     340     350

      370     380     390     400     410     420
/usr/t AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC
      :
AB0356 AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC
      360     370     380     390     400     410

      430     440     450     460     470     480
/usr/t AGGGGTCTGGCCCATCTCCATGCCCAAGGTGATCCATCGAGACATCAAGGGGCAGAAT
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## Exhibit A

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AB0356 AGGGGTCTGGCCCATCTCCATGCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT
      420      430      440      450      460      470

      490      500      510      520      530      540
/usr/t GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG
AB0356 GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG
      480      490      500      510      520      530

      550      560      570      580      590      600
/usr/t GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG
AB0356 GACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG
      540      550      560      570      580      590

      610      620      630      640      650      660
/usr/t GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT
AB0356 GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT
      600      610      620      630      640      650

      670      680      690      700      710      720
/usr/t CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGTGACATGCACCCC
AB0356 CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGTGACATGCACCCC
      660      670      680      690      700      710

      730      740      750      760      770      780
/usr/t ATGCGAGCCCTCTTCCTCATTCCCTCGGAACCCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG
AB0356 ATGCGAGCCCTCTTCCTCATTCCCTCGGAACCCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG
      720      730      740      750      760      770

      790      800      810      820      830      840
/usr/t TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA
AB0356 TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA
      780      790      800      810      820      830

      850      860      870      880      890      900
/usr/t CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC
AB0356 CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC
      840      850      860      870      880      890

      910      920      930      940      950      960
/usr/t CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG
AB0356 CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG
      900      910      920      930      940      950

      970      980      990      1000      1010      1020
/usr/t ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG
AB0356 ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG
      960      970      980      990      1000      1010

      1030      1040      1050      1060      1070      1080
/usr/t CCAAGCTCCATCATGAACGTGCCTGGAGAGTGCAGTCTACGCCGGGAGTTTCTCCGGCTC
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:
AB0356 CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC
      1020      1030      1040      1050      1060      1070

      1090      1100      1110      1120      1130      1140
/usr/t CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAACAGCAGCAGCAGCTGCAGCAGCAG
:
AB0356 CAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAACAGCAGCAGCAGCTGCAGCAGCAG
      1080      1090      1100      1110      1120      1130

      1150      1160      1170      1180      1190      1200
/usr/t CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA
:
AB0356 CAGCAGCGAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGGCAGCGGCGCATA
      1140      1150      1160      1170      1180      1190

      1210      1220      1230      1240      1250      1260
/usr/t GAGGAGCAGAAGGAGGAGCGGCGCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG
:
AB0356 GAGGAGCAGAAGGAGGAGCGGCGCGCGTGGAGGAGCAACAGCGGCGGGAGCGGGAGCAG
      1200      1210      1220      1230      1240      1250

      1270      1280      1290      1300      1310      1320
/usr/t CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG
:
AB0356 CGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAGGCTCTGCGGCGG
      1260      1270      1280      1290      1300      1310

      1330      1340      1350      1360      1370      1380
/usr/t GAGGAGGAGCGGCGGCAGGCGGAGCGTGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG
:
AB0356 GAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATACAAGCGGAAGCAGCTGGAGGAG
      1320      1330      1340      1350      1360      1370

      1390      1400      1410      1420      1430      1440
/usr/t CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC
:
AB0356 CAGCGGCAGTCAGAACGTCTCCAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCC
      1380      1390      1400      1410      1420      1430

      1450      1460      1470      1480      1490      1500
/usr/t CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT
:
AB0356 CTGCAGCAGCAGCAACAGCAGCAGCAGCTTCAGAAACAGCAGCAGCAGCAGCTCCTGCCT
      1440      1450      1460      1470      1480      1490

      1510      1520      1530      1540      1550      1560
/usr/t GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC
:
AB0356 GGGGACAGGAAGCCCCTGTACCATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCC
      1500      1510      1520      1530      1540      1550

      1570      1580      1590      1600      1610      1620
/usr/t TGGGCCCCGAGAGGTAGAAGAGAGAAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC
:
AB0356 TGGGCCCCGAGAGGTAGAAGAGAGAAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCC
      1560      1570      1580      1590      1600      1610

      1630      1640      1650      1660      1670      1680
/usr/t AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCCC
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:
AB0356 AAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCCCCATCCCCAGGCCCTCCCCAGGGCCC
      1620      1630      1640      1650      1660      1670

      1690      1700      1710      1720      1730      1740
/usr/t CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG
:
AB0356 CCAGGACCCCTTTCCCAGACTCCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCG
      1680      1690      1700      1710      1720      1730

/usr/t CACAAG-----
:
AB0356 CACAAGAGCCTGGTGGCACACCGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGA
      1740      1750      1760      1770      1780      1790

      1750      1760      1770      1780      1790      1800
/usr/t -----TCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC
:
AB0356 TCCAGTCCCTGCAGGACCAGCCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGAC
      1800      1810      1820      1830      1840      1850

      1810      1820      1830      1840      1850      1860
/usr/t CCGGACCCCTGCCATCCCCGCACCCACTGCCACGCCAGTGCCCGAGGAGCTGTCATCCGC
:
AB0356 CCGGACCCCTGCCATCCCCGCACCCACTGCCACGCCAGTGCCCGAGGAGCTGTCATCCGC
      1860      1870      1880      1890      1900      1910

      1870      1880      1890      1900      1910      1920
/usr/t CAGAATTCAGACCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC
:
AB0356 CAGAATTCAGACCCACCTCTGAAGGACCTGGCCCCAGCCCGAATCCCCCAGCCTGGGTC
      1920      1930      1940      1950      1960      1970

      1930      1940      1950      1960      1970      1980
/usr/t CGCCCAGATAACGAGGCCCCACCCAAGGTGCCCTCAGAGGACCTCATCTATCGCCACTGCC
:
AB0356 CGCCCAGATAACGAGGCCCCACCCAAGGTGCCCTCAGAGGACCTCATCTATCGCCACTGCC
      1980      1990      2000      2010      2020      2030

      1990      2000      2010      2020      2030      2040
/usr/t CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCAGGCAGTCCGTGCCAGACCTCGC
:
AB0356 CTTAACACCAGTGGGGCCGGAGGGTCCCGGCCAGCCAGGCAGTCCGTGCCAG-----
      2040      2050      2060      2070      2080

      2050      2060      2070      2080      2090      2100
/usr/t AGCAACTCCGCCTGGCAAATCTATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCT
AB0356 -----

      2110      2120      2130      2140      2150      2160
/usr/t CCAGGGCCCCCTGCTCAGCCCCCTGGCCCCGCCAACGCCTCTAGTAACCCCGACCTCAGG
:
AB0356 -----TAACCCCGACCTCAGG
                                2090      2100

      2170      2180      2190      2200      2210      2220
/usr/t AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC

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:
AB0356 AGGAGCGACCCTGGCTGGGAACGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTC
      2110      2120      2130      2140      2150      2160
      2230      2240      2250      2260      2270      2280
/usr/t CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGCCTCCTCCAAACTGGACAGCTCC
:
AB0356 CCCCAGGCTGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCCTCCAAACGGACAGCTCC
      2170      2180      2190      2200      2210      2220
      2290      2300      2310      2320      2330      2340
/usr/t CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCGACGACCACCGCTCACGGCCAGGCCGG
:
AB0356 CCTGTGCTCTCCCCTGGGAATAAAGCCAAGCCGACGACCACCGCTCACGGCCAGGCCGG
      2230      2240      2250      2260      2270      2280
      2350      2360      2370      2380      2390      2400
/usr/t CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCTCGGCCTCCCAAG
:
AB0356 CCCGCAGACTTTGTGTTGCTGAAAGAGCGGACTCTGGACGAGGCCCTCGGCCTCCCAAG
      2290      2300      2310      2320      2330      2340
      2410      2420      2430      2440      2450      2460
/usr/t AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG
:
AB0356 AAGGCCATGGACTACTCGTCGTCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAG
      2350      2360      2370      2380      2390      2400
      2470      2480      2490      2500      2510      2520
/usr/t GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGAGCGATGGG
:
AB0356 GAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGAGATACCCCTGGGGGCCGAGCGATGGG
      2410      2420      2430      2440      2450      2460
      2530      2540      2550      2560      2570      2580
/usr/t GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG
:
AB0356 GATACAGACAGCGTCAGCACCATGGTGGTCCACGACGTCGAGGAGATCACCGGGACCCAG
      2470      2480      2490      2500      2510      2520
      2590      2600      2610      2620      2630      2640
/usr/t CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG
:
AB0356 CCCCCATACGGGGGCGGCACCATGGTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTG
      2530      2540      2550      2560      2570      2580
      2650      2660      2670      2680      2690      2700
/usr/t CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA
:
AB0356 CTGCATGCTGACAGCAATGGGTACACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCA
      2590      2600      2610      2620      2630      2640
      2710      2720      2730      2740      2750      2760
/usr/t CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG
:
AB0356 CCCACCGAGAACAGCAAAGGCCAAAGCCCACCCTCGAAGGATGGGAGTGGTGACTACCAG
      2650      2660      2670      2680      2690      2700
      2770      2780      2790      2800      2810      2820
/usr/t TCTCGTGGGCTGGTAAAGGCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG
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:
AB0356 TCTCGTGGGCTGGTAAAGGCCCTGGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGG
      2710      2720      2730      2740      2750      2760

      2830      2840      2850      2860      2870      2880
/usr/t ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG
:
AB0356 ATCTACCAGCCTGGAGGCAGTGGGGACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAG
      2770      2780      2790      2800      2810      2820

      2890      2900      2910      2920      2930      2940
/usr/t GGCACCTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTCTGTGGTCAACGTGAAT
:
AB0356 GGCACCTCGGCTCGACCAGCTGCAGTACGACGTGAGGAAGGGTCTGTGGTCAACGTGAAT
      2830      2840      2850      2860      2870      2880

      2950      2960      2970      2980      2990      3000
/usr/t CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCT
:
AB0356 CCCACCAACACCCGGGCCCACAGTGAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCT
      2890      2900      2910      2920      2930      2940

      3010      3020      3030      3040      3050      3060
/usr/t AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC
:
AB0356 AACTCCGAGATCCTCTGTGCAGCCCTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAAC
      2950      2960      2970      2980      2990      3000

      3070      3080      3090      3100      3110      3120
/usr/t GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA
:
AB0356 GGGCTGATGTTGCTGGACCGAAGTGGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGA
      3010      3020      3030      3040      3050      3060

      3130      3140      3150      3160      3170      3180
/usr/t CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA
:
AB0356 CGCTTCCAGCAGATGGATGTGCTGGAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAA
      3070      3080      3090      3100      3110      3120

      3190      3200      3210      3220      3230      3240
/usr/t AGGAACAAACTGCGGGTGTATTACCTGTCTGGCTCCGGAACAAGATTCTGCACAATGAC
:
AB0356 AGGAACAAACTGCGGGTGTATTACCTGTCTGGCTCCGGAACAAGATTCTGCACAATGAC
      3130      3140      3150      3160      3170      3180

      3250      3260      3270      3280      3290      3300
/usr/t CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC
:
AB0356 CCAGAAGTGGAGAAGAAGCAGGGCTGGACCACCGTGGGGGACATGGAGGGCTGCGGGCAC
      3190      3200      3210      3220      3230      3240

      3310      3320      3330      3340      3350      3360
/usr/t TACCGTGTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG
:
AB0356 TACCGTGTGTGAAATACGAGCGGATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTG
      3250      3260      3270      3280      3290      3300

      3370      3380      3390      3400      3410      3420
/usr/t GAGGTGTATGCCTGGGCCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC
```

```

AB0356 GAGGTGTATGCCTGGGCCCCAAACCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCC
      3310      3320      3330      3340      3350      3360
      3430      3440      3450      3460      3470      3480
/usr/t GACCTCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG
      3370      3380      3390      3400      3410      3420
AB0356 GACCTCCCCACCGCCCTCTGCTGGTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAG
      3370      3380      3390      3400      3410      3420
      3490      3500      3510      3520      3530      3540
/usr/t GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTGCGACTCGGGGAACAGCTAT
      3430      3440      3450      3460      3470      3480
AB0356 GTCATCTATGGCTCCAGTGCTGGCTTCCATGCTGTGGATGTGCGACTCGGGGAACAGCTAT
      3430      3440      3450      3460      3470      3480
      3550      3560      3570      3580      3590      3600
/usr/t GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC
      3490      3500      3510      3520      3530      3540
AB0356 GACATCTACATCCCTGTGCACATCCAGAGCCAGATCACGCCCCATGCCATCATCTTCCTC
      3490      3500      3510      3520      3530      3540
      3610      3620      3630      3640      3650      3660
/usr/t CCGAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC
      3550      3560      3570      3580      3590      3600
AB0356 CCGAACACCGACGGCATGGAGATGCTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAAC
      3550      3560      3570      3580      3590      3600
      3670      3680      3690      3700      3710      3720
/usr/t ACGTACGGGCGCATCATTAAAGGATGTGGTGCTGCAGTGGGGGAGATGCCTACTTCTGTG
      3610      3620      3630      3640      3650      3660
AB0356 ACGTACGGGCGCATCATTAAAGGATGTGGTGCTGCAGTGGGGGAGATGCCTACTTCTGTG
      3610      3620      3630      3640      3650      3660
      3730      3740      3750      3760      3770      3780
/usr/t GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT
      3670      3680      3690      3700      3710      3720
AB0356 GCCTACATCTGCTCCAACCAGATAATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCT
      3670      3680      3690      3700      3710      3720
      3790      3800      3810      3820      3830      3840
/usr/t GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC
      3730      3740      3750      3760      3770      3780
AB0356 GTGGAGACGGGCCACCTCGACGGGGTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTC
      3730      3740      3750      3760      3770      3780
      3850      3860      3870      3880      3890      3900
/usr/t CTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA
      3790      3800      3810      3820      3830      3840
AB0356 CTGTGTGAGCGGAATGACAAGGTGTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAA
      3790      3800      3810      3820      3830      3840
      3910      3920      3930      3940      3950
/usr/t GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTGAAAGGGC
      3850      3860      3870      3880
AB0356 GTTTACTTCATGACTCTGAACCGTAACTGCATCATGAACTGGTG-----
      3850      3860      3870      3880
```

Elapsed time: 0:00:07



## Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds) Q8N4C8

G

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GenBank/GenPept

Entrez

### Revision history for Q8N4C8

#### Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

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Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

Check sequence revision history

How to create WWW links to Entrez

LinkOut

Cubby

GI	Version	Update Date	Status	I	II
29427834	n/a	<a href="#">Oct 12 2004 10:54 AM</a>	Live	<input checked="" type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Sep 14 2004 10:15 AM</a>	Dead	<input type="radio"/>	<input checked="" type="radio"/>
29427834	n/a	<a href="#">Aug 17 2004 9:52 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Jun 23 2004 2:26 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">May 25 2004 9:58 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Apr 16 2004 10:20 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Mar 19 2004 11:02 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Sep 2 2003 8:23 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Jul 29 2003 8:28 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Jul 1 2003 8:14 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
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29427834	n/a	<a href="#">Apr 15 2003 8:13 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>
29427834	n/a	<a href="#">Apr 1 2003 8:10 AM</a>	Dead	<input type="radio"/>	<input type="radio"/>

Accession Q8N4C8 was first seen at NCBI on Apr 1 2003 8:10 AM

#### Related resources

BLAST

Reference sequence project

LocusLink

Clusters of orthologous groups

Protein reviews on the web

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[NCBI](#) | [NLM](#) | [NIH](#)

## Exhibit B

# Align two sequences

Mon Nov 29 23:10:56 "GMT 2004

```
/usr/tmp/seq1.292377.sca : 1312 aa
>SEQ ID NO:2, 1312 bases, B7C6E48A checksum.      1312 aa vs.
>AB035698, 1295 bases, DE542880 checksum.        1295 aa
scoring matrix: , gap penalties: -12/-2
95.6% identity;      Global alignment score: 8500
```

```

      10      20      30      40      50      60
/usr/t MGD PAPARSLDDIDLSALRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE
      .....
AB0356 MGD PAPARSLDDIDLSALRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE
      10      20      30      40      50      60

      70      80      90     100     110     120
/usr/t DEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSPPGNDDQLWLVMFCGAGSVTDLVKNT
      .....
AB0356 DEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSPPGNDDQLWLVMFCGAGSVTDLVKNT
      70      80      90     100     110     120

      130     140     150     160     170     180
/usr/t KGNALKEDCIAYICREILRGLAHLHAHKVIHRDIKGQNVLLTENA EVKLVD FGVSAQLDR
      .....
AB0356 KGNALKEDCIAYICREILRGLAHLHAHKVIHRDIKGQNVLLTENA EVKLVD FGVSAQLDR
      130     140     150     160     170     180

      190     200     210     220     230     240
/usr/t TVGRNTFIGTPYWMAPEVIACDENPDATYDYSRDIWSLGITAEIEMAEGAPPLCDMHPMR
      .....
AB0356 TVGRNTFIGTPYWMAPEVIACDENPDATYDYSRDIWSLGITAEIEMAEGAPPLCDMHPMR
      190     200     210     220     230     240

      250     260     270     280     290     300
/usr/t ALFLIPRNPPRLKSKKWSKKFIDFIDTCLIKTYLSRPPTEQLLKFPFIRDQPTERQVRI
      .....
AB0356 ALFLIPRNPPRLKSKKWSKKFIDFIDTCLIKTYLSRPPTEQLLKFPFIRDQPTERQVRI
      250     260     270     280     290     300

      310     320     330     340     350     360
/usr/t QLKDHIDRSRKKRGEKEETEY EYSGSEEDDSHGEEGEPSSIMNVPGESTLRREFLRLQQ
      .....
AB0356 QLKDHIDRSRKKRGEKEETEY EYSGSEEDDSHGEEGEPSSIMNVPGESTLRREFLRLQQ
      310     320     330     340     350     360

      370     380     390     400     410     420
/usr/t ENKSNSEALKQQQQQLQQQQQ RDPEAHIKHLLHQRRRIEEQKEERRRV EEQRREREQRK
      .....
AB0356 ENKSNSEALKQQQQQLQQQQQ RDPEAHIKHLLHQRRRIEEQKEERRRV EEQRREREQRK
      370     380     390     400     410     420

      430     440     450     460     470     480
/usr/t LQEKEQQRRL EDMQALRREEERRQAEREQEYKRKQLEEQRQSERLQRQLQ QEHAYLKS LQ
```

## Exhibit C

11/29/2004



```

:
AB0356 EILCAALWGVNLLVGTENGLMLLDRSGQGKVYGLIGRRRFQQMDVLEGLNLLITISGKRN
      990      1000      1010      1020      1030      1040

      1070      1080      1090      1100      1110      1120
/usr/t KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEV
:
AB0356 KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEV
      1050      1060      1070      1080      1090      1100

      1130      1140      1150      1160      1170      1180
/usr/t YAWAPKPYHKFMAFKSFADLPHRPLLVDLTVEEGQRLKVIYGSSAGFHAVDSDSGNSYDI
:
AB0356 YAWAPKPYHKFMAFKSFADLPHRPLLVDLTVEEGQRLKVIYGSSAGFHAVDSDSGNSYDI
      1110      1120      1130      1140      1150      1160

      1190      1200      1210      1220      1230      1240
/usr/t YIPVHIQSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRIIKDVVLQWGEMPTSVAY
:
AB0356 YIPVHIQSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRIIKDVVLQWGEMPTSVAY
      1170      1180      1190      1200      1210      1220

      1250      1260      1270      1280      1290      1300
/usr/t ICSNQIMGWGEKAIEIRSVETGHLDGVMHKRAQRLKFLCERNDKVFFASVRSGGSSQVY
:
AB0356 ICSNQIMGWGEKAIEIRSVETGHLDGVMHKRAQRLKFLCERNDKVFFASVRSGGSSQVY
      1230      1240      1250      1260      1270      1280

      1310
/usr/t FMTLNRNCIMNW
:
AB0356 FMTLNRNCIMNW
      1290
```

Elapsed time: 0:00:00

# Align two sequences

**Tue Nov 30 19:27:20 "GMT 2004**

```
/usr/tmp/seq1.293861.sca : 3951 nt
>SEQ ID NO:1, 3951 bases, A90814F5 checksum.      3951 nt vs.
>SEQ ID NO:11 US Pat. '716 , 4133 bases, 5AD89B50 4133 nt
scoring matrix: , gap penalties: -12/-2
90.2% identity;      Global alignment score: 14405
```

```

      10      20      30      40      50      60
/usr/t GCCCTTATGGGCGACCCAGCCCCGCCCGCAGCCTGGACGACATCGACCTGTCCGCCCTG
      ::      ::
SEQ    GC-----AT-----

      70      80      90      100     110     120
/usr/t CGGGACCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGTCGGCAATGGAACCTACGGACAG
      ::      ::      ::      ::      ::      ::
SEQ    -----TTGGGGAGGTG-----
              10

      130     140     150     160     170     180
/usr/t GTGTACAAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC
      ::      ::      ::      ::      ::      ::
SEQ    ---TATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAGGTCATGGATGTC
      20      30      40      50      60      70

      190     200     210     220     230     240
/usr/t ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC
      ::      ::      ::      ::      ::      ::
SEQ    ACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCAC
      80      90      100     110     120     130

      250     260     270     280     290     300
/usr/t CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGAAACGAT
      ::      ::      ::      ::      ::      ::
SEQ    CACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGAAACGAT
      140     150     160     170     180     190

      310     320     330     340     350     360
/usr/t GACCAGCTCTGGCTGGTGTAGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG
      ::      ::      ::      ::      ::      ::
SEQ    GACCAGCTCTGGCTGGTGTAGGAGTTCTGTGGTGCTGGTTCAGTGACTGACCTGGTAAAG
      200     210     220     230     240     250

      370     380     390     400     410     420
/usr/t AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC
      ::      ::      ::      ::      ::      ::
SEQ    AACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGCAGGGAGATCCTC
      260     270     280     290     300     310

      430     440     450     460     470     480
/usr/t AGGGGTCTGGCCCATCTCCATGCCCAAGGTGATCCATCGAGACATCAAGGGGCAGAAT
```

## Exhibit D

```

      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    AGGGGTCTGGCCCATCTCCATGCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAAT
      320      330      340      350      360      370

      490      500      510      520      530      540
/usr/t GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCTG
      380      390      400      410      420      430

      550      560      570      580      590      600
/usr/t GACCGCACCGTGGGCAGACGGAACACTTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GACCGCACCGTGGGCAGACGGAACACTTTTCATTGGGACTCCCTACTGGATGGCTCCAGAG
      440      450      460      470      480      490

      610      620      630      640      650      660
/usr/t GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGTGATATTTGGTCT
      500      510      520      530      540      550

      670      680      690      700      710      720
/usr/t CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGTGACATGCACCCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    CTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGTGACATGCACCCC
      560      570      580      590      600      610

      730      740      750      760      770      780
/usr/t ATGCGAGCCCTCTTCCTCATTTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    ATGCGAGCCCTCTTCCTCATTTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGG
      620      630      640      650      660      670

      790      800      810      820      830      840
/usr/t TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    TCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAGCCGCCCA
      680      690      700      710      720      730

      850      860      870      880      890      900
/usr/t CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    CCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACGGAGCGGCAGGTC
      740      750      760      770      780      790

      910      920      930      940      950      960
/usr/t CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    CGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGTGAGAAAGAGGAG
      800      810      820      830      840      850

      970      980      990      1000      1010      1020
/usr/t ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    ACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGAGAGGAAGGAGAG
      860      870      880      890      900      910

      1030      1040      1050      1060      1070      1080
/usr/t CCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAGTTTCTCCGGCTC
```

11/30/2004

```

      .....
SEQ  GGCATGAATCCCGCTGACAAACCAGCCTGGGCCCGAGAGGTAGAAGAGAGAACAAGGATG
      1520      1530      1540      1550      1560      1570

      1600      1610      1620      1630      1640      1650
/usr/t AACAAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCC
      .....
SEQ  AACAAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACGGGGCCTGAGCCC
      1580      1590      1600      1610      1620      1630

      1660      1670      1680      1690      1700      1710
/usr/t CCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCAGACTCCTCCTATGCAG
      .....
SEQ  CCCATCCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCAGACTCCTCCTATGCAG
      1640      1650      1660      1670      1680      1690

      1720      1730      1740
/usr/t AGGCCGGTGGAGCCCCAGGAGGGACCGCACAAAG-----
      .....
SEQ  AGGCCGGTGGAGCCCCAGGAGGGACCGCACAAAGCCTGGTGGCACACCGGGTCCCCTG
      1700      1710      1720      1730      1740      1750

      1750      1760      1770
/usr/t -----TCCCTGCAGGACCAGCCCACCCGAAAC
      .....
SEQ  AAGCCATATGCAGCACCTGTACCCCGATCCCAGTCCCTGCAGGACCAGCCCACCCGAAAC
      1760      1770      1780      1790      1800      1810

      1780      1790      1800      1810      1820      1830
/usr/t CTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCCTGCCATCCCCGCACCCACTGCCACG
      .....
SEQ  CTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCCTGCCATCCCCGCACCCACTGCCACG
      1820      1830      1840      1850      1860      1870

      1840      1850      1860      1870      1880      1890
/usr/t CCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTTCAGACCCACCTCTGAAGGACCTGGC
      .....
SEQ  CCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTTCAGACCCACCTCTGAAGGACCTGGC
      1880      1890      1900      1910      1920      1930

      1900      1910      1920      1930      1940      1950
/usr/t CCCAGCCCGAATCCCCCAGCCTGGGTCCGCCAGATAACGAGGCCCCACCCAAGGTGCCT
      .....
SEQ  CCCAGCCCGAATCCCCCAGCCTGGGTCCGCCAGATAACGAGGCCCCACCCAAGGTGCCT
      1940      1950      1960      1970      1980      1990

      1960      1970      1980      1990      2000      2010
/usr/t CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGAGGGTCCCGGCCA
      .....
SEQ  CAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGAGGGTCCCGGCCA
      2000      2010      2020      2030      2040      2050

      2020      2030      2040      2050      2060      2070
/usr/t GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGG
      .....
SEQ  GCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATCTATCTGCAAAGG
      2060      2070      2080      2090      2100      2110

      2080      2090      2100      2110      2120      2130
/usr/t CGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCGCCC
```

```

      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    CGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCCCCTGGCCCCGCC
      2120      2130      2140      2150      2160      2170

      2140      2150      2160      2170      2180      2190
/usr/t AACGCCTCTAGTAACCCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    AACGCCTCTAGTAACCCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAACGCTCGGACAGC
      2180      2190      2200      2210      2220      2230

      2200      2210      2220      2230      2240      2250
/usr/t GTCCTTCCAGCCTCTCACGGGCACCTCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GTCCTTCCAGCCTCTCACGGGCACCTCCCCAGGCTGGCTCACTGGAGCGGAACCGCGTG
      2240      2250      2260      2270      2280      2290

      2260      2270      2280      2290      2300      2310
/usr/t GGAGCCTCCTCCAAACTGGACAGCTCCCCGTGTGCTCTCCCCTGGAATAAAGCCAAGCCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GGAGTCTCCTCCAAACCGGACAGCTCCCCGTGTGCTCTCCCCTGGAATAAAGCCAAGCCC
      2300      2310      2320      2330      2340      2350

      2320      2330      2340      2350      2360      2370
/usr/t GACGACCACCGCTCACGGCCAGGCCGCGCCGCGAGACTTTGTGTTGCTGAAAGAGCGGACT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GACGACCACCGCTCACGGCCAGGCCGCGCCGCGAGACTTTGTGTTGCTGAAAGAGCGGACT
      2360      2370      2380      2390      2400      2410

      2380      2390      2400      2410      2420      2430
/usr/t CTGGACGAGGCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCAGCGAGGAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    CTGGACGAGGCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCGTCAGCGAGGAG
      2420      2430      2440      2450      2460      2470

      2440      2450      2460      2470      2480      2490
/usr/t GTGGAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GTGGAAGCAGTGAGGACGACGAGGAGGAAGGCGAAGGCGGGCCAGCAGAGGGGAGCAGA
      2480      2490      2500      2510      2520      2530

      2500      2510      2520      2530      2540      2550
/usr/t GATACCCCTGGGGGGCCGCGAGCGATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCAC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GATACCCCTGGGGGGCCGC---GATGGGGATACAGACAGCGTCAGCACCATGGTGGTCCAC
      2540      2550      2560      2570      2580

      2560      2570      2580      2590      2600      2610
/usr/t GACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    GACGTCGAGGAGATCACCGGGACCCAGCCCCCATACGGGGGCGGCACCATGGTGGTCCAG
      2590      2600      2610      2620      2630      2640

      2620      2630      2640      2650      2660      2670
/usr/t CGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    CGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTACACAAACCTG
      2650      2660      2670      2680      2690      2700

      2680      2690      2700      2710      2720      2730
/usr/t CCTGACGTGGTCCAGCCCAGCCACTACCCACCGAGAACAGCAAAGGCCAAAGCCCACCC
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      .....
SEQ    CCTGACGTGGTCCAGCCCAGCCACTACCCACCGAGAACAGCAAAGGCCAAAGCCCACCC
      2710      2720      2730      2740      2750      2760

      2740      2750      2760      2770      2780      2790
/usr/t  TCGAAGGATGGGAGTGGTGA CTACAGTCTCGTGGGCTGGTAAAGGCCCTGGCAAGAGC
      .....
SEQ    TCGAAGGATGGGAGTGGTGA CTACAGTCTCGTGGGCTGGTAAAGGCCCTGGCAAGAGC
      2770      2780      2790      2800      2810      2820

      2800      2810      2820      2830      2840      2850
/usr/t  TCGTTACAGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATC
      .....
SEQ    TCGTTACAGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGGGACAGCATC
      2830      2840      2850      2860      2870      2880

      2860      2870      2880      2890      2900      2910
/usr/t  CCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTG
      .....
SEQ    CCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAGTACGACGTG
      2890      2900      2910      2920      2930      2940

      2920      2930      2940      2950      2960      2970
/usr/t  AGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCT
      .....
SEQ    AGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCCACAGTGAGACCCCT
      2950      2960      2970      2980      2990      3000

      2980      2990      3000      3010      3020      3030
/usr/t  GAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGG
      .....
SEQ    GAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCCCTTTGGGGG
      3010      3020      3030      3040      3050      3060

      3040      3050      3060      3070      3080      3090
/usr/t  GTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGC
      .....
SEQ    GTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGTGGGCAGGGC
      3070      3080      3090      3100      3110      3120

      3100      3110      3120      3130      3140      3150
/usr/t  AAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTC
      .....
SEQ    AAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTGGAGGGGCTC
      3130      3140      3150      3160      3170      3180

      3160      3170      3180      3190      3200      3210
/usr/t  AACCTGCTCATCACCATCTCAGGGAAGGAACAACTGCGGGTGTATTACCTGTCCTGG
      .....
SEQ    AACCTGCTCATCACCATCTCAGGGAAGGAACAACTGCGGGTGTATTACTTGTCTCTGG
      3190      3200      3210      3220      3230      3240

      3220      3230      3240      3250      3260      3270
/usr/t  CTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACC
      .....
SEQ    CTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGCTGGACCACC
      3250      3260      3270      3280      3290      3300

      3280      3290      3300      3310      3320      3330
/usr/t  GTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTGTGAAATACGAGCGGATTAAGTTC

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      .....
SEQ   GTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTGTGAAATACGAGCGGATTAAGTTC
      3310      3320      3330      3340      3350      3360

      3340      3350      3360      3370      3380      3390
/usr/t CTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCAC
      .....
SEQ   CTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAAACCCTACCAC
      3370      3380      3390      3400      3410      3420

      3400      3410      3420      3430      3440      3450
/usr/t AAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCACCGCCCTCTGCTGGTCGACCTG
      .....
SEQ   AAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCACCGCCCTCTGCTGGTCGACCTG
      3430      3440      3450      3460      3470      3480

      3460      3470      3480      3490      3500      3510
/usr/t ACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCT
      .....
SEQ   ACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGCTTCCATGCT
      3490      3500      3510      3520      3530      3540

      3520      3530      3540      3550      3560      3570
/usr/t GTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAG
      .....
SEQ   GTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATCCAGAGCCAG
      3550      3560      3570      3580      3590      3600

      3580      3590      3600      3610      3620      3630
/usr/t ATCAGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGC
      .....
SEQ   ATCAGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATGCTGCTGTGC
      3610      3620      3630      3640      3650      3660

      3640      3650      3660      3670      3680      3690
/usr/t TACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAAGGATGTGGTGCTG
      .....
SEQ   TACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAAGGATGTGGTGCTG
      3670      3680      3690      3700      3710      3720

      3700      3710      3720      3730      3740      3750
/usr/t CAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGG
      .....
SEQ   CAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATAATGGGCTGG
      3730      3740      3750      3760      3770      3780

      3760      3770      3780      3790      3800      3810
/usr/t GGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATG
      .....
SEQ   GGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGGGTCTTCATG
      3790      3800      3810      3820      3830      3840

      3820      3830      3840      3850      3860      3870
/usr/t CACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCC
      .....
SEQ   CACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTGTTTTTTGCC
      3850      3860      3870      3880      3890      3900

      3880      3890      3900      3910      3920      3930
/usr/t TCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACTGCATC

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      .....
SEQ   TCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGTAACCGCATC
      3910      3920      3930      3940      3950      3960

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      3940      3950
/usr/t ATGAACTGGTCAAAGGGC-----
      .....
SEQ   ATGAACTGGTGACGGGGCCCTGGGCTGGGGCTGTCCCACACTGGACCCAGCTCTCCCCCT
      3970      3980      3990      4000      4010      4020

```

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/usr/t -----
SEQ   GCAGCCAGGCTTCCCGGGCCGCCCTCTTTCCCTCCCTGGGCTTTTGCTTTTACTGGTT
      4030      4040      4050      4060      4070      4080

```

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/usr/t -----
SEQ   TGATTTCACTGGAGCCTGCTGGGAACGTGACCTCTGACCCCTGA
      4090      4100      4110      4120      4130

```

Elapsed time: 0:00:08

## Align two sequences



Mon Nov 29 23:45:09 "GMT 2004

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/usr/tmp/seq1.291680.sca : 1312 aa
>SEQ ID NO:2, 1312 bases, B7C6E48A checksum.      1312 aa vs.
>SEQ ID NO:15 '716 pat, 1326 bases, BB9CFAFC chec 1326 aa
scoring matrix: , gap penalties: -12/-2
93.3% identity;      Global alignment score: 8439

```

```

      10      20      30      40      50      60
/usr/t MGD PAPARSLDDIDLSALRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE
SEQ -----AFGEVYEGRHVKTGQLAAIKVMDVTE
                        10      20

      70      80      90     100     110     120
/usr/t DEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSPPGNDDQLWLVMFCGAGSVTDLVKNT
SEQ DEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSPPGNDDQLWLVMFCGAGSVTDLVKNT
      30      40      50      60      70      80

     130     140     150     160     170     180
/usr/t KGNALKEDCIAYICREILRGLAHLHAHKVIHRDIKGQNVLLTENA EVKLVD FGVSAQLDR
SEQ KGNALKEDCIAYICREILRGLAHLHAHKVIHRDIKGQNVLLTENA EVKLVD FGVSAQLDR
      90     100     110     120     130     140

     190     200     210     220     230     240
/usr/t TVGRRNTFIGTPYWMAPEVIACDENPDATYDYSRDIWSLGITAIEMAEGAPPLCDMHPMR
SEQ TVGRRNTFIGTPYWMAPEVIACDENPDATYDYSRDIWSLGITAIEMAEGAPPLCDMHPMR
     150     160     170     180     190     200

     250     260     270     280     290     300
/usr/t ALFLIPRNPPPRPKSKKWSKKFIDFIDTCLIKTYLSRPPTEQLLKFPFIRDQPTERQVRI
SEQ ALFLIPRNPPPRPKSKKWSKKFIDFIDTCLIKTYLSRPPTEQLLKFPFIRDQPTERQVRI
     210     220     230     240     250     260

     310     320     330     340     350     360
/usr/t QLKDHIDRSRKKRGEKEETEY EYSGSEEEEDSHGEEGEPSSIMNVPGESTLRREFLRLQQ
SEQ QLKDHIDRSRKKRGEKEETEY EYSGSEEEEDSHGEEGEPSSIMNVPGESTLRREFLRLQQ
     270     280     290     300     310     320

     370     380     390     400     410     420
/usr/t ENKSNSEALKQQQQQLQQQQQORDPEAHIKHLLHQRRRIEEQKEERRRVEEQQRREREQRK
SEQ ENKSNSEALKQQQQQLQQQQQORDPEAHIKHLLHQRRRIEEQKEERRRVEEQQRREREQRK
     330     340     350     360     370     380

     430     440     450
/usr/t LQEKEQQRRLEDMQALRREEERRQAEREQEY-----

```

**Exhibit E**

11/29/2004

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:.....
SEQ  GSVVNVNPTNTRAHSETPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKV
      990      1000      1010      1020      1030      1040

      1040      1050      1060      1070      1080      1090
/usr/t YGLIGRRRFQQMDVLEGLNLLITISGKRNLRVYYLSWLRNKILHNDPEVEKKQGWTTVG
:.....
SEQ  YGLIGRRRFQQMDVLEGLNLLITISGKRNLRVYYLSWLRNKILHNDPEVEKKQGWTTVG
      1050      1060      1070      1080      1090      1100

      1100      1110      1120      1130      1140      1150
/usr/t DMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSFADLPHRPLLVDLTV
:.....
SEQ  DMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSFADLPHRPLLVDLTV
      1110      1120      1130      1140      1150      1160

      1160      1170      1180      1190      1200      1210
/usr/t EEGQRLKVIYGSSAGFHAVDVDSGNSYDIYIPVHIQSQITPHAIIFLPNTDGMEMLLCYE
:.....
SEQ  EEGQRLKVIYGSSAGFHAVDVDSGNSYDIYIPVHIQSQITPHAIIFLPNTDGMEMLLCYE
      1170      1180      1190      1200      1210      1220

      1220      1230      1240      1250      1260      1270
/usr/t DEGVYVNTYGRIIKDVLQWGEMPTSVAYICSNQIMGWGEKAIEIRSVETGHLDDGVFMHK
:.....
SEQ  DEGVYVNTYGRIIKDVLQWGEMPTSVAYICSNQIMGWGEKAIEIRSVETGHLDDGVFMHK
      1230      1240      1250      1260      1270      1280

      1280      1290      1300      1310
/usr/t RAQRLKFLCERNDKVFFASVRSGGSSQVYFMTLNRNCIMNW
:.....
SEQ  RAQRLKFLCERNDKVFFASVRSGGSSQVYFMTLNRNRIMNW
      1290      1300      1310      1320

```

Elapsed time: 0:00:00